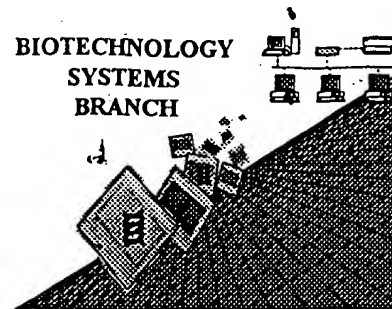


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



0590
1204

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/993,292
Source: 01K
Date Processed by STIC: 12/3/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

Does Not Comply
Corrected Diskette Needed

Error on p. 5

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4 <110> APPLICANT: James E. Galen
5 University of Maryland
7 <120> TITLE OF INVENTION: USE OF CLY A HEMOLYSIN FOR EXCRETION OF
8 PROTEINS
10 <130> FILE REFERENCE: UOFMD.007A
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/993,292
C--> 12 <141> CURRENT FILING DATE: 2001-11-23
12 <150> PRIOR APPLICATION NUMBER: 60/252,516
13 <151> PRIOR FILING DATE: 2000-11-22
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 6271
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: pSEC84 Expression Plasmid
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30 taaagttaat gatgatagcg ggagttattc tagttgcgag tgaaggtttt gttttgacat 180
31 tcagtgtctgt caaatactta agaataagtt attgatttta accttgaatt attattgctt 240
32 gatgttaggt gcttatttcg ccattccgca ataacttaaa aaagttccct tgcatttaca 300
33 ttttgaaaca tctatagcga taaatgaaac atcttaaaaag ttttagtata atattcgtgt 360
34 tggattattc tgcatttttg gggagaatgg acttgccgac tgattaatga gggttaatca 420
35 gtatgcagtg gcataaaaaa gcaataaaag gcatataaca gatcgatctt aaacatccac 480
36 aggaggatgg gatccaaaat agggaggaaa aaaaaatgac tagtattttt gcagaacaaa 540
37 ctgtagaggt agttaaagc gcgatcgaaa ccgcagatgg ggcattagat ctttataaca 600
38 aataacctga ccaggtcatc ccctggaaga cctttgatga aaccataaaa gagttaagcc 660
39 gttttaaaca ggagtactcg caggaagctt ctgttttagt tggatgattt aaagttttgc 720
40 ttatggacag ccaggacaag tattttgaag cgacacaaaac tgtttatgaa tgggtgtggtg 780
41 tcgtgacgca attactctca gcgtatattt tactatttga tgaatataat gagaaaaaag 840
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43 aagcgcaaaa atctctcctg acaagttcac aaagtttcaa caacgcttcc ggaaaactgc 960
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56 tcatagctca cgctgtaggt atctcagttc ggtgtaggtc gttcgctcca agctgggctg 1740

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

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57 tgtgcacgaa cccccgttc agcccgaccg ctgcgcctta tccggtaact atcgtcttga 1800
58 gtccaacccg gtaagacacg acttatcgcc actggcagca gccactggta acaggattag 1860
59 cagagcgagg tatgtaggcg gtgctacaga gttcttgaag tgggtggccta actacggcta 1920
60 cactagaagg acagtatttg gtatctgcgc tctgctgaag ccagttacct tcggaaaaag 1980
61 agttggtagc tcttgatccg gcaaacaaac caccgctggt agcggtggtt tttttgtttg 2040
62 caagcagcag attacgcgca gaaaaaaagg atctcaagaa gatcctttga tcttttctac 2100
63 ggggtctgac gctcagtaga tctaaaacac taggcccaag agttttaga aacgcaaaaa 2160
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67 actgagcctt tcgttttatt tgatgcctgg cagtcccta ctctcgcatg gggagacccc 2400
68 aactaccat cggcgctacg gcgtttcact tctgagttcg gcatggggtc aggtgggacc 2460
69 accgcgctac tgccgccagg caaattctgt tttatcagac cgcttctgcg ttctgattta 2520
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77 tcaaccggat ctaaaacact agcccaacct ttcatagaag gcggcgggtg aatcgaaatc 3000
78 tcgtgatggc aggttggcg tcgcttggtc ggtcatttcg aacccagag tcccgcctag 3060
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90 cgcccctgcg ctgacagccg gaacacggcg gcatcagagc agccgattgt ctggtgtgcc 3780
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97 atgaaagcgg ccacctcct gtgtcgtct ctgtaacgaa tctcgcacag cgattttcgt 4200
98 gtcagataag tgaatatcaa cagtgtgaga cacacgatca acacacacca gacaagggaa 4260
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101 tatcttcttt ctgccacaca acacggcaac aaaccacctt cagtcatga ggcagaaagc 4440
102 ctcaagcgcc gggcacatca tagcccatat acctgcacgc tgaccacact cactttccct 4500
103 gaaaataatc cgctcattca gaccgttcac gggaaatccg tgtgattgtt gccgcatcac 4560
104 gctgcctccc ggagtttgtc tcgagcactt ttgttaccgg ccaaacaaaa ccaaaaaaca 4620
105 acccataccc aaccctaata aacacaaaaa caagacaaat aatcattgat tgatgggtga 4680

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RAW SEQUENCE LISTING

DATE: 12/03/2001

PATENT APPLICATION: US/09/993,292

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

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106 aatgggggttaa acttgacaaa caaacccact taaaacccaa aacataccca aacacacacc 4740
107 aaaaaaacac cataaggagt ttataaatg ttggtattca ttgatgacgg ttcaacaaac 4800
108 atcaaactac agtggcagga aagcgacgga acaattaaac agcacattag cccgaacagc 4860
109 ttcaaacgcg agtgggcagt ctcttttggg gataaaaagg tctttaacta cacactgaac 4920
110 ggcgaacagt attcatttga tccaatcagc ccggatgctg tagtcacaac caatatcgca 4980
111 tggcaatata gcgacgttaa tgcgttgca gtgcatacag ccttactgac cagtggctctg 5040
112 ccggtaaagc aagtggatat tgtttgcaca ctctctctga cagagtatta cgacagaaat 5100
113 aaccaaccca atacggaaaa tattgagcgt aagaaagcaa acttccggaa aaaaattaca 5160
114 ttaaatggcg gggatacatt cacaataaaa gatgtaaaag tcatgcctga atctataccg 5220
115 gcaggttatg aagttctaca agaactggat gagttagatt ctttattaat tatagatctc 5280
116 gggggcacca cattagatat ttctcaggta atggggaaat tatcggggat cagtaaaata 5340
117 tacggagact catctcttgg tgtctctctg gttacatctg cagtaaaaga tgccctttct 5400
118 cttgcgagaa caaaaggaag tagctatctt gctgacgata taatcattca cagaaaagat 5460
119 aataactatc tgaagcaacg aattaatgat gagaacaaaa tatcaatagt caccgaagca 5520
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121 ggttatactc atggtatggt tataggcggg ggcgcagaat taatatgcca tgcagtaaaa 5640
122 aaacacacac agattcgtga tgaacgtttt ttcaaaacca ataactctca atatgattta 5700
123 gttaacggta tgtatctcat aggtaatata tgatggacaa gcgcagaacc attgccttca 5760
124 aactaaatcc agatgtaaat caaacagata aaattgtttg tgatacactg gacagtatcc 5820
125 cgcaagggga acgaagccgc cttaaccggg ccgcactgac ggcaggtctg gccttatata 5880
126 gacaagatcc ccggacccct ttctttttat gtgagctgct gacgaaagaa accacatttt 5940
127 cagatatcgt gaatatattg agatcgctat ttccaaaaga gatggccgat tttaattctt 6000
128 caatagtcac tcaatcctct tcacaacaag agcaaaaaag tgatgaagag accaaaaaaa 6060
129 atgcgatgaa gctaataaat taattcaatt attattgagt tccctttatc cactatcagg 6120
130 ctggataaag ggaactcaat caagttattt tcttaccagt cattacataa tcgttattat 6180
131 gaaataatcg ttgcaactgt ctctgttatt caggcaattt caataaaggc acttgctcac 6240
132 gctctgtcat ttctgaaac tcttcatgct g 6271

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134 <210> SEQ ID NO: 2

135 <211> LENGTH: 305

136 <212> TYPE: PRT

137 <213> ORGANISM: Salmonella Typhi

139 <400> SEQUENCE: 2

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140 Met Thr Ser Ile Phe Ala Glu Gln Thr Val Glu Val Val Lys Ser Ala
141 1 5 10 15
142 Ile Glu Thr Ala Asp Gly Ala Leu Asp Leu Tyr Asn Lys Tyr Leu Asp
143 20 25 30
144 Gln Val Ile Pro Trp Lys Thr Phe Asp Glu Thr Ile Lys Glu Leu Ser
145 35 40 45
146 Arg Phe Lys Gln Glu Tyr Ser Gln Glu Ala Ser Val Leu Val Gly Asp
147 50 55 60
148 Ile Lys Val Leu Leu Met Asp Ser Gln Asp Lys Tyr Phe Glu Ala Thr
149 65 70 75 80
150 Gln Thr Val Tyr Glu Trp Cys Gly Val Val Thr Gln Leu Leu Ser Ala
151 85 90 95
152 Tyr Ile Leu Leu Phe Asp Glu Tyr Asn Glu Lys Lys Ala Ser Ala Gln
153 100 105 110
154 Lys Asp Ile Leu Ile Arg Ile Leu Asp Asp Gly Val Lys Lys Leu Asn
155 115 120 125
156 Glu Ala Gln Lys Ser Leu Leu Thr Ser Ser Gln Ser Phe Asn Asn Ala

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RAW SEQUENCE LISTING

DATE: 12/03/2001

PATENT APPLICATION: US/09/993,292

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

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157      130      135      140
158 Ser Gly Lys Leu Leu Ala Leu Asp Ser Gln Leu Thr Asn Asp Phe Ser
159 145      150      155      160
160 Glu Lys Ser Ser Tyr Phe Gln Ser Gln Val Asp Arg Ile Arg Lys Glu
161      165      170      175
162 Ala Tyr Ala Gly Ala Ala Ala Gly Ile Val Ala Gly Pro Phe Gly Leu
163      180      185      190
164 Ile Ile Ser Tyr Ser Ile Ala Ala Gly Val Ile Glu Gly Lys Leu Ile
165      195      200      205
166 Pro Glu Leu Asn Asn Arg Leu Lys Thr Val Gln Asn Phe Phe Thr Ser
167      210      215      220
168 Leu Ser Ala Thr Val Lys Gln Ala Asn Lys Asp Ile Asp Ala Ala Lys
169 225      230      235      240
170 Leu Lys Leu Ala Thr Glu Ile Ala Ala Ile Gly Glu Ile Lys Thr Glu
171      245      250      255
172 Thr Glu Thr Thr Arg Phe Tyr Val Asp Tyr Asp Asp Leu Met Leu Ser
173      260      265      270
174 Leu Leu Lys Gly Ala Ala Lys Lys Met Ile Asn Thr Cys Asn Glu Tyr
175      275      280      285
176 Gln Gln Arg His Gly Lys Lys Thr Leu Phe Glu Val Pro Asp Val Ala
177      290      295      300
178 Ser
179 305
182 <210> SEQ ID NO: 3
183 <211> LENGTH: 102
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: Cloning primer
190 <400> SEQUENCE: 3
191 ggatccaaaa taaggaggaa aaaaaaatga ctagtatttt tgcagaacaa actgtagagg 60
192 tagttaaaag cgcgatcgaa accgcgatg gggcattaga tc 102
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 101
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Cloning primer
202 <400> SEQUENCE: 4
203 cctagggttat cagctagcga cgtcaggaac ctcgaaaagc gtcttcttac catgacgttg 60
204 ttggtattca ttacaggtgt taatcatitt ctttgcagct c 101
206 <210> SEQ ID NO: 5
207 <211> LENGTH: 97
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: Cloning primer
214 <400> SEQUENCE: 5
215 cacggttaaga agacgctttt cgagggttcct gacgtcgcta gctgataacc taggtcatgt 60

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RAW SEQUENCE LISTING

DATE: 12/03/2001

PATENT APPLICATION: US/09/993,292

TIME: 12:19:47

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

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216 tagacagctt atcatcgata agctttaatg cggtagt 97
218 <210> SEQ ID NO: 6
219 <211> LENGTH: 69
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: Cloning primer
226 <400> SEQUENCE: 6
227 agatctacta gtgtcgacgc tagctatcag gtcgagggtgg cccgggtcca tgcaccgcga 60
228 cgcaacgcg 69
230 <210> SEQ ID NO: 7
231 <211> LENGTH: 60
232 <212> TYPE: DNA
233 <213> ORGANISM: Artificial Sequence
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Cloning primer
238 <400> SEQUENCE: 7
239 actagtcacc cagaaacgct ggtgaaagta aaagatgctg aagatcagtt ggggtgcacga 60
242 <210> SEQ ID NO: 8
243 <211> LENGTH: 101
244 <212> TYPE: DNA
245 <213> ORGANISM: Artificial Sequence
247 <220> FEATURE:
248 <223> OTHER INFORMATION: Cloning primer
250 <400> SEQUENCE: 8
251 cattaaggt tatcgatgat aagctgtcaa acatgagcta gcctaggtca ttaccaatgc 60
252 ttaatcagtg aggcacctat ctcagcgatc tgtctatttc g 101
254 <210> SEQ ID NO: 9
255 <211> LENGTH: 101
256 <212> TYPE: DNA
C--> 257 <213> ORGANISM: Artificial sequence
W--> 259 <220> FEATURE:
W--> 259 <223> OTHER INFORMATION:
259 <400> SEQUENCE: 9
260 cgaaatagac agatcgctga gatagggtgcc tcaactgatta agcattggta atgacctagg 60
261 ctagctcatg ttgacagct tatcatcgat aacctttaat g 101
263 <210> SEQ ID NO: 10
264 <211> LENGTH: 71
265 <212> TYPE: DNA
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Cloning primer
271 <400> SEQUENCE: 10
272 gcgcactagt aaagaaacga accaaaagcc atataaggaa acatacggca tttcccatat 60
273 tacacgcat g 71
275 <210> SEQ ID NO: 11
276 <211> LENGTH: 103
277 <212> TYPE: DNA
278 <213> ORGANISM: Artificial Sequence

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Explanation missing - see error summary sheet, item

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/993,292

DATE: 12/03/2001

TIME: 12:19:48

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\11212001\I993292.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:257 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9
L:259 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:259 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:525 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:19, CDS LOCATION: (0)...
(2253)

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/993,292

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☐ Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ Skipped Sequences
(OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ Skipped Sequences
(NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 9 ☒ Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☐ Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 ☒ Use of <220> Sequence(s) 9 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ PatentIn 2.0
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